



# SEQUENCE LISTING

<110> Short, Jay M.  
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Garrett, James B.  
O' Donoghue, Eileen  
Mathur, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES  
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<141> 2001-05-24

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<151> 2000-05-25

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<151> 1999-03-01

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<151> 1997-08-13

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Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
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aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu 65 70 75 80	240
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tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa	180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	229
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro	
1 5 10	
tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg	277
Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu	
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gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag	325
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys	
35 40 45	
gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg	373
Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp	
50 55 60	
ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc	421
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala	
65 70 75	
tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg	469
Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu	
80 85 90	
gcg aaa aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat	517
Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp	
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gtc gac gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg	565
Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu	
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gca cct gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt	613
Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser	
130 135 140	
ccc gat ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat	661
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp	
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Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile	
160 165 170	
gct gac ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg	757
Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg	
175 180 185 190	
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Val Leu Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln	
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gac gaa agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg	853
Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val	
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Ser Ala Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met	

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Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro			
240	245	250	
ggg tgg gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt			997
Gly Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser			
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ttg cat aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc			1045
Leu His Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala			
275	280	285	
cgc agc cgc gcc acc ccg tta tta gat ttg atc aag aca gcg ttg acg			1093
Arg Ser Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr			
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Pro His Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser			
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Val Leu Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly			
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Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys			
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Ser Leu			
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cggtgctggc gcgtttaatc acaccattga ggatagcgcc tttaatatg acgcctgcct			1713
gttcagacg ctgcattgac aaactcacct ctttggcgggt gttcaagcca aaacgcgcaa			1773
ccagcaggct ggtgccaaca gaacgccccca cgaccgcggc atcactcacc gccagcatcg			1833



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Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
35 40 45  
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
50 55 60  
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
65 70 75 80  
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
85 90 95  
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
100 105 110  
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
115 120 125  
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp  
130 135 140  
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala  
145 150 155 160  
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp  
165 170 175  
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu  
180 185 190  
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu  
195 200 205  
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala  
210 215 220  
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
225 230 235 240  
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp  
245 250 255  
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
260 265 270  
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser  
275 280 285  
Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His  
290 295 300  
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
305 310 315 320  
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
325 330 335  
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
340 345 350  
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
355 360 365  
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
370 375 380  
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
385 390 395 400

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<221> CDS  
<222> (1)...(1296)

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ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96  
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
20 25 30  
gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144  
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Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys  
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Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
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 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
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 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys  
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 Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
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 Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
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 245 250 255  
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
 260 265 270  
 Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser  
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 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His  
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# Appendix A:

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SEQ ID NO:9 (Nov9x) and SEQ ID NO:7 (AppA, or wild type) alignment

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	10	20	30	40	50	60	
Nov9x	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....						1
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	70	80	90	100	110	120	
Nov9x	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....						1
AppA	ctctccacccttgtgttggtatggctggaccgcgctctgaaaagttaacgaacgtaggcc						120
	130	140	150	160	170	180	
Nov9x	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....						1
AppA	tgatgcggcgcattagcatcgcacaggcaatcaataatgtcagatatgaaaagcggaaa						180
	190	200	210	220	230	240	
Nov9x	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....						53
AppA	catatcg	atgaaagcgatcttaatcccatTTTTTatctcttctgattccggttaaccccgca					240
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AppA	atctgcattcgcctcagagtgcgcggagctgaagctggaaagtgtggtgattgtcagtcg						300
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Nov9x	tcatgggtgtgcgtgctccaaccaaggccacgcaactgatgcaggatgtcaccccagacgc						173
AppA	tcatgggtgtgcgtgctccaaccaaggccacgcaactgatgcaggatgtcaccccagacgc						360
	370	380	390	400	410	420	
Nov9x	atggccaacctggccggtaaaactgggtgagctgacaccgcgcgggtggtgagctaatacgc						233
AppA	atggccaacctggccggtaaaactgggtgagctgacaccgcgcgggtggtgagctaatacgc						420
	430	440	450	460	470	480	
Nov9x	ctatctcggacattactggcgtcagcgtctggttagccgacggattgctgcttaaatgtgg						293
AppA	ctatctcggacattacaaacgcagcgtctggttagccgacggattgctgctgcaaaaagg						480
	490	500	510	520	530	540	
Nov9x	ctgcccgcagctctggtcaggtcgcgattattgctgatgtcgacgagcgtaccgtaaaac						353
AppA	ctgcccgcagctctggtcaggtcgcgattattgctgatgtcgacgagcgtaccgtaaaac						540
	550	560	570	580	590	600	
Nov9x	aggcgaagccttcgccgcgggctggcacctgactgtgcaataaccgtacatacccaggc						413
AppA	aggcgaagccttcgccgcgggctggcacctgactgtgcaataaccgtacatacccaggc						600
	610	620	630	640	650	660	
Nov9x	agatacgtccagtcgccgatccggtattttaatcctctaaaaactggcggttgccaactgga						473
AppA	agatacgtccagtcgccgatccggtattttaatcctctaaaaactggcggttgccaactgga						660
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[illegible]

# Appendix A:

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SEQ ID NO:9 (Nov9x) and SEQ ID NO:7 (AppA, or wild type) alignment

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Nov9x	tttacagcagatgCGTgataaaacgcCGctgtcattaaatacgccgcccggagaggtgaa	1193
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	1390 1400 1410 1420 1430 1440	
Nov9x	actgaccctggcaggatgtgaagagcgaaatgcgcagggcatgtgttcggtggcagggttt	1253
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	1450 1460 1470 1480 1490 1500	
Nov9x	tacgcaaatacgtgaatgaagcacgcataccggcgtgcagtttgagatctcatcaccatca	1313
AppA	tacgcaaatacgtgaatgaagcacgcataccggcgtgcagtttgtaatgcataaaaagag	1500
	1510 1520 1530 1540 1550 1560	
Nov9x	ccatcactaa	1323
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	1570 1580 1590 1600 1610 1620	
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	1750 1760 1770 1780 1790 1800	
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	1810 1820 1830 1840 1850 1860	
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	1870 1880 1890 1900	
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